

Input Set : A:\42711c11.app
Output Set: N:\CRF3\07252000\I483672A.raw

```

3 <110> APPLICANT: Xu, Jiangchun
4 Dillon, Davin C.
5 Mitcham, Jennifer L.
6 Harlocker, Susan Louise
7 Jiang Yuqui
8 Reed, Steven G.
9 Kalos, Michael D.
10 Fanger, Gary R.
11 Retter, Marc W.
12 Solk, John A.
13 Day, Craig H.
14 Skeiky, Yasir A.W.
15 Wang, Aijun
16 Meagher, Madeleine
18 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
19 DIAGNOSIS OF PROSTATE CANCER
21 <130> FILE REFERENCE: 210121.42711c11
C--> 23 <140> CURRENT APPLICATION NUMBER: US/09/483,672A
24 <141> CURRENT FILING DATE: 2000-01-14
26 <160> NUMBER OF SEQ ID NOS: 590
28 <170> SOFTWARE: FastSeq for Windows Version 3.0

```

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

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7200 <210> SEQ ID NO: 378
7201 <211> LENGTH: 1719
7202 <212> TYPE: PRT
7203 <213> ORGANISM: Homo sapien
7205 <400> SEQUENCE: 378
7206 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
7207 1 5 10 15
7208 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
7209 20 25 30
7210 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
7211 35 40 45
7212 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
7213 50 55 60
7214 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
7215 65 70 75 80
7216 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
7217 85 90 95
7218 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
7219 100 105 110
7220 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
7221 115 120 125
7222 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/483,672A

DATE: 07/25/2000
 TIME: 14:32:14

Input Set : A:\42711c11.app
 Output Set: N:\CRF3\07252000\I483672A.raw

```

7223      130      135      140
7224 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
7225 145      150      155      160
7226 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
7227      165      170      175
7228 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
7229      180      185      190
7230 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
7231      195      200      205
7232 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
7233      210      215      220
7234 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
7235 225      230      235      240
7236 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
7237      245      250      255
7238 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
7239      260      265      270
7240 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
7241      275      280      285
7242 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
7243      290      295      300
7244 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
7245 305      310      315      320
7246 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
7247      325      330      335
7248 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
7249      340      345      350
7250 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
7251      355      360      365
7252 Ser Ser Glu Asn Ser Asn Pro Glu Asn Val Ser Arg Thr Arg Asn Lys
7253      370      375      380
7254 Pro Arg Thr His Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser
7255 385      390      395      400
7256 Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys
7257      405      410      415
7258 Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly
7259      420      425      430
7260 Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys
7261      435      440      445
7262 Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly
7263      450      455      460
7264 Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys
7265 465      470      475      480
7266 Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys
7267      485      490      495
7268 Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp
7269      500      505      510
7270 Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu
7271      515      520      525

```

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```

7272 Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp
7273      530      535      540
7274 Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln
7275      545      550      555      560
7276 Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val
7277      565      570      575
7278 Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn
7279      580      585      590
7280 Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu
7281      595      600      605
7282 Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp
7283      610      615      620
7284 Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys
7285      625      630      635      640
7286 Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys
7287      645      650      655
7288 Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys
7289      660      665      670
7290 Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala
7291      675      680      685
7292 Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly
7293      690      695      700
7294 Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser
7295      705      710      715      720
7296 Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser
7297      725      730      735
7298 His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln
7299      740      745      750
7300 Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys
7301      755      760      765
7302 Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser
7303      770      775      780
7304 Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp
7305      785      790      795      800
7306 Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly
7307      805      810      815
7308 Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn
7309      820      825      830
7310 Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe
7311      835      840      845
7312 Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser
7313      850      855      860
7314 Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn
7315      865      870      875      880
7316 Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu
7317      885      890      895
7318 Glu Gly Ser Glu Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile
7319      900      905      910
7320 Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn

```

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```

7321          915          920          925
7322 Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro
7323          930          935          940
7324 Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu
7325 945          950          955          960
7326 Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe
7327          965          970          975
7328 Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His
7329          980          985          990
7330 Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser
7331          995          1000          1005
7332 Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu
7333          1010          1015          1020
7334 Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His
E--> 7335 1025          1030          1035          1040 1044
7336 Gln Ser Gln Leu Pro Arg Thr His Met Val Val Glu Val Asp Ser Met
7337          1045          1050          1055
7338 Pro Ala Ala Ser Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met
7339          1060          1065          1070
7340 Gly Lys Trp Cys Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys
7341          1075          1080          1085
7342 Ser Asn Val Gly Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr
7343          1090          1095          1100
7344 Leu Arg Ser Lys Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys
E--> 7345 1105          1110          1115          1120 1120
7346 Arg Gly Ser Gly Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp
7347          1125          1130          1135
7348 Ser Ala Met Lys Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His
7349          1140          1145          1150
7350 Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp
7351          1155          1160          1165
7352 Gly Asp Tyr Asp Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg
7353          1170          1175          1180
7354 Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val
E--> 7355 1185          1190          1195          1200 1200
7356 Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys
7357          1205          1210          1215
7358 Lys Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly
7359          1220          1225          1230
7360 Asn Ser Glu Val Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn
7361          1235          1240          1245
7362 Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys
7363          1250          1255          1260
7364 Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro
E--> 7365 1265          1270          1275          1280 1280
7366 Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr
7367          1285          1290          1295
7368 Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp
7369          1300          1305          1310

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```

7370 Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val
7371      1315      1320      1325
7372 His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala
7373      1330      1335      1340
7374 Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala
E--> 7375 1345      1350      1355      136
7376 Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn
7377      1365      1370      1375
7378 Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr
7379      1380      1385      1390
7380 Ala Val Ser Ser His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr
7381      1395      1400      1405
7382 Lys Glu Lys Gln Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu
7383      1410      1415      1420
7384 Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly
E--> 7385 1425      1430      1435      144
7386 Ser Glu Asn Ser Gln Pro Glu Lys Met Ser Ser Gln Glu Pro Glu Ile Asn
7387      1445      1450      1455
7388 Lys Asp Gly Asp Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser
7389      1460      1465      1470
7390 Asn Asn Val Gly Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly
7391      1475      1480      1485
7392 Asn Gly Asp Asn Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu
7393      1490      1495      1500
7394 Asn Gln Gln Phe Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys
E--> 7395 1505      1510      1515      152
7396 Glu Leu Val Ser Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser
7397      1525      1530      1535
7398 Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu
7399      1540      1545      1550
7400 Ser Gln Arg Leu Glu Gly Ser Glu Asn Gly Gln Pro Glu Lys Arg Ser
7401      1555      1560      1565
7402 Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Leu Glu Asn Phe
7403      1570      1575      1580
7404 Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe
E--> 7405 1585      1590      1595      160
7406 Pro Glu Asn Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly
7407      1605      1610      1615
7408 Leu Ile Pro Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro
7409      1620      1625      1630
7410 Asp Thr Glu Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln
7411      1635      1640      1645
7412 Lys Gln Phe Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile
7413      1650      1655      1660
7414 Leu Ile His Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser
E--> 7415 1665      1670      1675      168
7416 Glu Leu Ser Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn
7417      1685      1690      1695
7418 Ser Thr Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr

```

same
Hyper J. enon

RAW SEQUENCE LISTING

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Input Set : A:\42711c11.app

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```

7419          1700          1705          1710
7420 Met Lys His Gln Ser Gln Leu
7421          1715
10356 <210> SEQ ID NO: 525
10357 <211> LENGTH: 254
10358 <212> TYPE: PRT
10359 <213> ORGANISM: Homo sapien
10361 <400> SEQUENCE: 525
10362 Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile
10363 1          5          10          15
10364 Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile
10365          20          25          30
10366 Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu
10367          35          40          45
10368 Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln
10369          50          55          60
10370 Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly
10371 65          70          75          80
10372 Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
10373          85          90          95
10374 Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu
10375          100         105         110
10376 Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu
10377          115         120         125
10378 Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala
10379          130         135         140
10380 Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg
10381 145         150         155         160
10382 Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu
10383          165         170         175
10384 Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys
10385          180         185         190
10386 Ala Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly
10387          195         200         205
10388 Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly
10389          210         215         220
10390 Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu
10391 225         230         235         240
10392 Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
E--> 10393 245 250

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misaligned nos

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Input Set : A:\42711c11.app
Output Set: N:\CRF3\07252000\I483672A.raw

L:23 M:270 C: Current Application Number differs, Wrong Format
L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:51 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:53 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:54 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:77 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:78 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:80 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:97 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:131 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:227 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:230 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

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Input Set : A:\42711c11.app
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L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:698 M:283 W: Missing Blank Line separator, <210> field identifier
L:1467 M:283 W: Missing Blank Line separator, <400> field identifier
L:7335 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:378
M:332 Repeated in SeqNo=378
L:10018 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502
L:10018 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502
L:10018 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502
L:10018 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502
L:10018 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:502
L:10019 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502
L:10019 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502
L:10019 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502
L:10019 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502
M:340 Repeated in SeqNo=502
L:10020 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502
L:10020 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502
L:10020 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502
L:10020 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502
L:10021 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502
L:10021 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502
L:10021 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502
L:10021 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502
L:10023 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502
L:10023 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502
L:10023 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502
L:10023 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502
L:10031 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503
L:10031 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503
L:10031 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503
L:10031 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503
L:10031 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:503
L:10032 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503
L:10032 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503
L:10032 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503
L:10032 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503
M:340 Repeated in SeqNo=503
L:10033 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503
L:10033 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503
L:10033 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503
L:10033 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503
L:10035 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503
L:10035 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503
L:10035 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503
L:10035 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503
L:10036 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503
L:10036 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503

VERIFICATION SUMMARY

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TIME: 14:32:16

Input Set : A:\42711c11.app

Output Set: N:\CRF3\07252000\I483672A.raw

L:10036 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503
L:10036 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503
L:10037 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503
L:10037 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503
L:10037 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503
L:10037 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503
L:10107 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:508
L:10107 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:508
L:10107 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:508
L:10107 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:508
L:10107 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:508
L:10393 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:525